SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Glutamine Amidotransferase Homologs

<130> BB1129

<140>
<141>

<150> 60/107,275
<151> 1998-11-05

<160> 15

<170> Microsoft Office 97

<210> 1
<211> 1956
<212> DNA
<213> Impatiens balsamia

<400> 1
gcacgagaag gaactggcaa gtaccaagcc acagaatggg ttcagaattc gcgccgcctt 60
ggctggtgca ggcggagatt ctgtggtgac tttacttgat tacggtgctg gaaatgttag 120
gagtgtgagg aacgccatcc gcacacttgg atttgatatc aaagatgtgc aaaagccaga 180
ggatattcta aatgctaagc gccttatctt tcctggcgtt ggggcctttg cacctgcaat 240
ggatgttctt attcgtaaag ggctggctga agcactctgt acttacattc agaatgatcg 300
acctttcctg ggtatatgcc tgggattgca gctactcttt gagtcaagtg aagaaaatgg 360
tccaattcaa ggtcttggct tgattcctgg acgggttggg cgttttgaat catccaatgg 420
tttaagggtg ccacatattg gatggcatgc cttggatata aaggaagggt cagcaatttt 480
agatgatgtg gggaatcaac atgtgtattt tgttcactca tatcgagcca atgccgagga 540
caacaaagag tggatttcat ctacatgcag ctatggtgac gattttattg catccattca 600
gaagggaaat gttcatgcag tccaatttca tcccgagaag agtggaggtg ttggactttc 660
catattgaga agatttttga atgctgattc ctttaacaac aaaagacaga agccaatgaa 720
tggaaaggct tctaaacttg caaagagagt aattgcttgc cttgatgtga gggcaaatga 780
taatggggat cttgttgtaa ccaagggaga ccaatatgat gtgagagaac gtacagaaga 840
gaatgaggtc agaaaccttg gcaagcctgt tgaacttgct gggcagtatt atttagacgg 900
tgctgatgag gtcagcttct taaacattac tggtttccgg gacttccctc taggcgatct 960
acccatgcta caggtcttgc aacgcgcatc tgaaaacgtt tttgtgccat taactgtcgg 1020
gggtggcatc agggatttta ctgatgcaaa tggaaggtat tattctagtc tagaagtggc 1080
ttcagagtat ttcagatcgg gcgccgataa ggtttcgatc ggaagtgatg cagtttacac 1140
tgctgaggaa tatattaaaa ccggagtgaa gacaggaaag agcagcatag agcagatatc 1200
tacagtatat ggtaaccagg cagtggttgt aagcattgat cctcgccgag tttacttgag 1260
aaaacccgat gaagtagaat ttaaagccat caaagtaagc catccaggtc caaacggtga 1320
ggaatatgcc tggtatcagt gcactgttaa tggtggacga gaagggagac ccatcggagc 1380
ttatgaacta gctaaggctg ttgaggaact tggagctgga gaaatattat tgaactgcat 1440
tgattgtgat ggtcaaggaa aaggattcga tatagatctg atcaagctaa tatccgatgc 1500
tgtgaacatt cctgttatcg caagcagcgg tgcaggagtc gctgatcact tctccgaagt 1560
ctttaatgaa accaacgcat ctgctgccct tgcagctggc attttccatc gcaaagaggt 1620
tccaattaag gctgttaaag agcacttgtt gaaggaaggg attgaagtta gattgtaagg 1680
cgagaatcac ttggaagaaa tttcatcttg aagttcaatt ttgttacaca agagatttcc 1740
ttctttcttg gcctatgtga tatttattta tttatgtttt gctattgaat tattgttatt 1800
attattttgg catttgttat ttgaatagat ttgagttttt agaccttggt gtgtcctgtt 1860
tatctctagg ccatgttttg tggattatat acaagtgtga aattaaataa ataaatcgta 1920
tgaatttatg cttttaaaaa aaaaaaaaaa aaaaaa 1956

<210> 2
<211> 558

<212> PRT
<213> Impatiens balsamia

<400> 2

```
His Glu Lys Glu Leu Ala Ser Thr Lys Pro Gln Asn Gly Phe Arg Ile
  1               5                  10                  15

Arg Ala Ala Leu Ala Gly Ala Gly Gly Asp Ser Val Val Thr Leu Leu
             20                  25                  30

Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn Ala Ile Arg Thr
         35                  40                  45

Leu Gly Phe Asp Ile Lys Asp Val Gln Lys Pro Glu Asp Ile Leu Asn
     50                  55                  60

Ala Lys Arg Leu Ile Phe Pro Gly Val Gly Ala Phe Ala Pro Ala Met
 65                  70                  75                  80

Asp Val Leu Ile Arg Lys Gly Leu Ala Glu Ala Leu Cys Thr Tyr Ile
                 85                  90                  95

Gln Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu Gln Leu Leu
            100                 105                 110

Phe Glu Ser Ser Glu Glu Asn Gly Pro Ile Gln Gly Leu Gly Leu Ile
        115                 120                 125

Pro Gly Arg Val Gly Arg Phe Glu Ser Ser Asn Gly Leu Arg Val Pro
    130                 135                 140

His Ile Gly Trp His Ala Leu Asp Ile Lys Glu Gly Ser Ala Ile Leu
145                 150                 155                 160

Asp Asp Val Gly Asn Gln His Val Tyr Phe Val His Ser Tyr Arg Ala
                165                 170                 175

Asn Ala Glu Asp Asn Lys Glu Trp Ile Ser Ser Thr Cys Ser Tyr Gly
            180                 185                 190

Asp Asp Phe Ile Ala Ser Ile Gln Lys Gly Asn Val His Ala Val Gln
        195                 200                 205

Phe His Pro Glu Lys Ser Gly Gly Val Gly Leu Ser Ile Leu Arg Arg
    210                 215                 220

Phe Leu Asn Ala Asp Ser Phe Asn Asn Lys Arg Gln Lys Pro Met Asn
225                 230                 235                 240

Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu Asp Val
                245                 250                 255

Arg Ala Asn Asp Asn Gly Asp Leu Val Val Thr Lys Gly Asp Gln Tyr
            260                 265                 270

Asp Val Arg Glu Arg Thr Glu Glu Asn Glu Val Arg Asn Leu Gly Lys
        275                 280                 285

Pro Val Glu Leu Ala Gly Gln Tyr Tyr Leu Asp Gly Ala Asp Glu Val
    290                 295                 300
```

```
Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly Asp Leu
305                 310                 315                 320

Pro Met Leu Gln Val Leu Gln Arg Ala Ser Glu Asn Val Phe Val Pro
                325                 330                 335

Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Asn Gly Arg
            340                 345                 350

Tyr Tyr Ser Ser Leu Glu Val Ala Ser Glu Tyr Phe Arg Ser Gly Ala
        355                 360                 365

Asp Lys Val Ser Ile Gly Ser Asp Ala Val Tyr Thr Ala Glu Glu Tyr
    370                 375                 380

Ile Lys Thr Gly Val Lys Thr Gly Lys Ser Ser Ile Glu Gln Ile Ser
385                 390                 395                 400

Thr Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro Arg Arg
                405                 410                 415

Val Tyr Leu Arg Lys Pro Asp Glu Val Glu Phe Lys Ala Ile Lys Val
            420                 425                 430

Ser His Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln Cys Thr
        435                 440                 445

Val Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala
    450                 455                 460

Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile
465                 470                 475                 480

Asp Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Ile Lys Leu
                485                 490                 495

Ile Ser Asp Ala Val Asn Ile Pro Val Ile Ala Ser Ser Gly Ala Gly
            500                 505                 510

Val Ala Asp His Phe Ser Glu Val Phe Asn Glu Thr Asn Ala Ser Ala
        515                 520                 525

Ala Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Lys Ala
    530                 535                 540

Val Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Leu
545                 550                 555
```

<210> 3
<211> 587
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (495)

<220>
<221> unsure
<222> (518)

<220>
<221> unsure
<222> (577)

<220>
<221> unsure
<222> (582)

<400> 3
aagaaaaggc ccgctagggc gccgagacag cggaacgttc tctgagtttg agcacgatct 60
ccccgggccc cggcgccgcc gtacgtcccc cttcggcgtc gccagccgcc tcctggctcc 120
ggctccttca tcgcctgctc cagcgtgcct gcgtgacata agcgtcgatt gattggcgag 180
aaaggggacg aatgcagccg ccgttgcagg cgcagggagc aatggctaac gtcgccgcta 240
tcctcaccgt cccctgctcc gcgggccgcc gcccgaagcg gagcaaccag ccccgcggat 300
gcggctccgt ctccgtctcc gtctccgtcc gtgcgtcctc cggcgcaaac acggtgactc 360
tgctggacta cggcgcgggg aacgtacgca gcgtgcgcaa cgcaattcgc tacctcggct 420
tcgacatccg cgacgtgcag agcccggarg acatcgtcgc cggcggaayg ggtcgtcttt 480
cccggtgtcg gcgcnttcgg ctccgccatg gacgtccnca ccaggacggg catgccaacg 540
cactccgtga gtacatccaa agggaacgcc ccttccnagg cnctgcc 587

<210> 4
<211> 130
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (90)

<220>
<221> UNSURE
<222> (93)

<220>
<221> UNSURE
<222> (109)

<220>
<221> UNSURE
<222> (115)

<220>
<221> UNSURE
<222> (129)

<400> 4
Met Gln Pro Pro Leu Gln Ala Gln Gly Ala Met Ala Asn Val Ala Ala
1 5 10 15

Ile Leu Thr Val Pro Cys Ser Ala Gly Arg Arg Pro Lys Arg Ser Asn
20 25 30

Gln Pro Arg Gly Cys Gly Ser Val Ser Val Ser Val Ser Val Arg Ala
35 40 45

```
Ser Ser Gly Ala Asn Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn
     50                  55                  60

Val Arg Ser Val Arg Asn Ala Ile Arg Tyr Leu Gly Phe Asp Ile Arg
 65                  70                  75                  80

Asp Val Gln Ser Pro Glu Asp Ile Val Xaa Ala Glu Xaa Val Val Phe
                85                  90                  95

Pro Gly Val Gly Ala Phe Gly Ser Ala Met Asp Val Xaa Thr Arg Thr
            100                 105                 110

Gly Met Xaa Asn Ala Leu Arg Glu Tyr Ile Gln Arg Glu Arg Pro Phe
        115                 120                 125

Xaa Gly
    130
```

<210> 5
<211> 1084
<212> DNA
<213> Zea mays

<400> 5

```
actagtggta acaaaaggcg atcaatatga tgtaagagat catactagca gcaaagaggt   60
aagaaacctt ggcaagccag tcgatttagc aagccagtac tacatagacg gtgctgatga  120
ggtcagcttc ttgaatataa ctggtttccg tgactttcca ttgggtgatt tgccaatgct  180
agaggtactg cgttgtgcct ctgaaaaggt ttttgtgcca cttacagttg gtgggggcat  240
acgagacttc acagatgcaa atggaagata ctactcaagt ttggaggtag catcagaata  300
tttcaggtcc ggtgctgaca aaatttcaat tggaagtgat gctgtttatg ctgctgaagc  360
ctttttacag actggtgtaa agacagggaa aagcagcttg gagcaaatct ctagagtata  420
tggcaatcag gctgtagttg tcagtattga tcctcgacgg gtatatgtca aaagtcaaga  480
agatgtgcca tttaaaactg taaaggtgtc cactaaaggt ccatcgggag aagaatatgc  540
atggtaccag tgcacagtga atggtggacg tgatagccga gctataggag catatgaact  600
agcgaaagct gtggaagaat tgggcgcagg agaaatactt cttaactgca ttgattgtga  660
tggccaaggt tgtggatttg acatagattt ggttaaaatg gtttctgatg ctgtgacaat  720
ccctgtcatt gcgagcagtg gtgctggagc tgttcaacat ttttctgaaa tttttgagaa  780
aacaaatgct tctgctgccc ttgctgctgg cattttccac cggaaagagg ttcctatact  840
agcagtgaaa gagcatctgg tcaatgctgg tgtggaggtc agggtgtaac agggagatcc  900
ttcggtttat tgaaatattc ttgtttgatg tcacaactgc tatcagttct gtttctctga  960
tgtcgcaact gctatcagat ctgttggtgg cagctggcag tgcataggcc cctgtcgaga 1020
actgcagttt ggtaataaat taataatgtg atgcttaaca gattaaaaaa aaaaaaaaaa 1080
aaaa                                                               1084
```

<210> 6
<211> 295
<212> PRT
<213> Zea mays

<400> 6

```
Leu Val Val Thr Lys Gly Asp Gln Tyr Asp Val Arg Asp His Thr Ser
  1               5                  10                  15

Ser Lys Glu Val Arg Asn Leu Gly Lys Pro Val Asp Leu Ala Ser Gln
             20                  25                  30

Tyr Tyr Ile Asp Gly Ala Asp Glu Val Ser Phe Leu Asn Ile Thr Gly
         35                  40                  45
```

```
Phe Arg Asp Phe Pro Leu Gly Asp Leu Pro Met Leu Glu Val Leu Arg
     50                  55                  60

Cys Ala Ser Glu Lys Val Phe Val Pro Leu Thr Val Gly Gly Gly Ile
 65                  70                  75                  80

Arg Asp Phe Thr Asp Ala Asn Gly Arg Tyr Tyr Ser Ser Leu Glu Val
                 85                  90                  95

Ala Ser Glu Tyr Phe Arg Ser Gly Ala Asp Lys Ile Ser Ile Gly Ser
            100                 105                 110

Asp Ala Val Tyr Ala Ala Glu Ala Phe Leu Gln Thr Gly Val Lys Thr
        115                 120                 125

Gly Lys Ser Ser Leu Glu Gln Ile Ser Arg Val Tyr Gly Asn Gln Ala
    130                 135                 140

Val Val Val Ser Ile Asp Pro Arg Arg Val Tyr Val Lys Ser Gln Glu
145                 150                 155                 160

Asp Val Pro Phe Lys Thr Val Lys Val Ser Thr Lys Gly Pro Ser Gly
                165                 170                 175

Glu Glu Tyr Ala Trp Tyr Gln Cys Thr Val Asn Gly Gly Arg Asp Ser
            180                 185                 190

Arg Ala Ile Gly Ala Tyr Glu Leu Ala Lys Ala Val Glu Glu Leu Gly
        195                 200                 205

Ala Gly Glu Ile Leu Leu Asn Cys Ile Asp Cys Asp Gly Gln Gly Cys
    210                 215                 220

Gly Phe Asp Ile Asp Leu Val Lys Met Val Ser Asp Ala Val Thr Ile
225                 230                 235                 240

Pro Val Ile Ala Ser Ser Gly Ala Gly Ala Val Gln His Phe Ser Glu
                245                 250                 255

Ile Phe Glu Lys Thr Asn Ala Ser Ala Ala Leu Ala Ala Gly Ile Phe
            260                 265                 270

His Arg Lys Glu Val Pro Ile Leu Ala Val Lys Glu His Leu Val Asn
        275                 280                 285

Ala Gly Val Glu Val Arg Val
    290                 295
```

<210> 7
<211> 494
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (6)

<220>
<221> unsure
<222> (12)

<220>
<221> unsure
<222> (43)

<220>
<221> unsure
<222> (56)

<220>
<221> unsure
<222> (60)

<220>
<221> unsure
<222> (154)..(155)

<220>
<221> unsure
<222> (161)

<220>
<221> unsure
<222> (163)

<220>
<221> unsure
<222> (166)

<220>
<221> unsure
<222> (202)

<220>
<221> unsure
<222> (215)

<220>
<221> unsure
<222> (266)

<220>
<221> unsure
<222> (271)

<220>
<221> unsure
<222> (274)..(275)

<220>
<221> unsure
<222> (277)

<220>
<221> unsure
<222> (306)

<220>
<221> unsure
<222> (320)

<220>
<221> unsure
<222> (346)..(347)

<220>
<221> unsure
<222> (356)

<220>
<221> unsure
<222> (393)

<220>
<221> unsure
<222> (434)

<220>
<221> unsure
<222> (441)

<220>
<221> unsure
<222> (456)

<220>
<221> unsure
<222> (466)

<220>
<221> unsure
<222> (474)

<400> 7
tcgggncccg gngattcccg gggtcgagcc aacgggtccg gtncctcaaa caaggncggn 60
catggtcaac gcactccggt ggagtatatc caagagggac cggccccttc ctaggcatct 120
gcctcggtct ccagctgctc ttcggattcc agcnnggaga nanggnccgt gtgagcggac 180
tcggtgtgat atcaggcgtg gncaggcgat tcgantcctc aaatggcctc atagttccac 240
atgttggctg gaacgctctc cagatnacca nggnnanacc actgttgcag ggagctgatg 300
gccagnatgt gtacttttgn tcactcctac cgcgtactgg cttcanngtg ctagtnagga 360
aactgggggt tcctccatat ggcaactatg ggngacagct tttaatcctc catctcaaat 420
ggggcaacat tcanggcaag ntcaaatttc acccangaaa agagtnggaa gctncccggg 480
actttcctat tcct 494

<210> 8
<211> 86
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (23)

<220>
<221> UNSURE
<222> (25)..(26)..(27)

<220>
<221> UNSURE
<222> (39)

<220>
<221> UNSURE
<222> (43)

<220>
<221> UNSURE
<222> (60)

<220>
<221> UNSURE
<222> (62)..(63)..(64)

<220>
<221> UNSURE
<222> (74)

<220>
<221> UNSURE
<222> (78)

<400> 8

```
Tyr Pro Arg Gly Thr Gly Pro Phe Leu Gly Ile Cys Leu Gly Leu Gln
  1               5                  10                  15

Leu Leu Phe Gly Phe Gln Xaa Gly Xaa Xaa Xaa Arg Val Ser Gly Leu
             20                  25                  30

Gly Val Ile Ser Gly Val Xaa Arg Arg Phe Xaa Ser Ser Asn Gly Leu
         35                  40                  45

Ile Val Pro His Val Gly Trp Asn Ala Leu Gln Xaa Thr Xaa Xaa Xaa
     50                  55                  60

Pro Leu Leu Gln Gly Ala Asp Gly Gln Xaa Val Tyr Phe Xaa His Ser
 65                  70                  75                  80

Tyr Arg Val Leu Ala Ser
                85
```

<210> 9
<211> 495
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (125)

<220>
<221> unsure
<222> (266)

<220>
<221> unsure
<222> (315)

<220>
<221> unsure
<222> (366)

<220>
<221> unsure
<222> (405)

<220>
<221> unsure
<222> (441)

<220>
<221> unsure
<222> (443)

<220>
<221> unsure
<222> (445)

<220>
<221> unsure
<222> (453)

<220>
<221> unsure
<222> (458)

<220>
<221> unsure
<222> (461)

<220>
<221> unsure
<222> (475)

<220>
<221> unsure
<222> (480)

<220>
<221> unsure
<222> (492)

<220>
<221> unsure
<222> (494)

<400> 9
gacacacacc ccccatactg ccacaagggc cgccgccgcc gccgggagcg atggtcgccg 60
ccacctccat caacgccgtc ccctgctccg ctggtcggcc gaagcggagg agccagcgcc 120
gcggngcctc tacggtcgcc gtgcgcgcgt ccggcgacgc tagcaccgtg acgctgctgg 180
actacggcgc gggcaacgtg cgcagcgtgc gcaatgccat ccgccacctc ggtttcggca 240
tccgcgacgt gcgcagcccg gagganatcc tcgccgccga ccgcctcgtc ttcccggggg 300
tcggcgcctt cgggntcaag ccatggacgt cctcaacccg ctccgggatg ggcggacgcg 360
cttccncgga gtacatccgg caggggaccg ccccccttcct cgggnatctg gccttcgggg 420
cttccaagct tctccttccg nantnctaag ggnaaggnag naattggccc cggtnaggcn 480
gggcttgggg tntnt 495

<210> 10
<211> 87
<212> PRT
<213> Oryza sativa

<220>
<221> UNSURE
<222> (72)

<400> 10
Met Val Ala Ala Thr Ser Ile Asn Ala Val Pro Cys Ser Ala Gly Arg
1 5 10 15

Pro Lys Arg Arg Ser Gln Arg Arg Gly Ala Ser Thr Val Ala Val Arg
20 25 30

Ala Ser Gly Asp Ala Ser Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly
35 40 45

Asn Val Arg Ser Val Arg Asn Ala Ile Arg His Leu Gly Phe Gly Ile
50 55 60

Arg Asp Val Arg Ser Pro Glu Xaa Ile Leu Ala Ala Asp Arg Leu Val
65 70 75 80

Phe Pro Gly Val Gly Ala Phe
85

<210> 11
<211> 178
<212> DNA
<213> Glycine max

<400> 11
ttgtgacttt gcttgattac ggtgctggca atgttcggag tgtcaggaat gcaatcagat 60
tcctcgggtt tgacataaaa gatgtgcaaa ctccgcaaga tattctgaat gcaagtcggt 120
tagtttttcc tggtgttgga gcatttgctg ctgccatgga ggtgttaagc aaaactgg 178

<210> 12
<211> 58
<212> PRT
<213> Glycine max

<400> 12
Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn
1 5 10 15

Ala Ile Arg Phe Leu Gly Phe Asp Ile Lys Asp Val Gln Thr Pro Gln
20 25 30

Asp Ile Leu Asn Ala Ser Arg Leu Val Phe Pro Gly Val Gly Ala Phe
35 40 45

Ala Ala Ala Met Glu Val Leu Ser Lys Thr
50 55

<210> 13
<211> 671
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (276)

<400> 13
gtatgtaaag gatcctaatg atgtgcaatt gaagaccata agggtttcaa gtccaggttc 60
aaatggagag gaatatgcat ggtatcaatg tacagttaat gggggacgag agggccggcc 120
aattggtgct tatgaactag caaaagcagt tgaagagctt ggtgctggtg aaatactact 180
taattgcatt gattgcgacg gtcaagggaa aggatttgat gtagatttaa ttaagttgat 240
atcaaatgct gtaagtatcc ctgttatcgc aagtancggt gctggtgctc ctgaacactt 300
ctctgaggtg ttctataaaa caaatgcatc agcagcactt gctgctggca tttttcacag 360
gaaagaggtg cctattcagt cggtaaaaga gcatttgttg aaggaaggca tagaagttcg 420
aatctgatca tatgcattta gtggtaaaat ttttgagatg cacttcataa taatcaaacc 480
ttgtacgtta tccctttttg tgtaatctaa cgaagctctc aaaatgtcaa ccttttggat 540
catgaaaaga ttttcacaac gagacctttc ctttgtaata tttttaagga aaatatattt 600
accatgtgca gcactatctc tgaacatttg ttattacaaa attatttcat gtgtcaaaaa 660
aaaaaaaaaa a 671

<210> 14
<211> 141
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (92)

<400> 14
Tyr Val Lys Asp Pro Asn Asp Val Gln Leu Lys Thr Ile Arg Val Ser
1 5 10 15

Ser Pro Gly Ser Asn Gly Glu Glu Tyr Ala Trp Tyr Gln Cys Thr Val
20 25 30

Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala Lys
35 40 45

Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile Asp
50 55 60

Cys Asp Gly Gln Gly Lys Gly Phe Asp Val Asp Leu Ile Lys Leu Ile
65 70 75 80

Ser Asn Ala Val Ser Ile Pro Val Ile Ala Ser Xaa Gly Ala Gly Ala
85 90 95

Pro Glu His Phe Ser Glu Val Phe Tyr Lys Thr Asn Ala Ser Ala Ala
100 105 110

Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Gln Ser Val
115 120 125

Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Ile
130 135 140

<210> 15
<211> 593
<212> PRT
<213> Arabidopsis thaliana

<400> 15
Met Glu Ala Thr Ala Ala Pro Phe Ser Ser Ile Val Ser Ser Arg Gln
1 5 10 15

```
Asn Phe Ser Ser Ser Ser Ser Ile Arg Ala Ser Ser Pro Ala Ser Leu
            20                  25                  30

Phe Leu Ser Gln Lys Ser Ile Gly Asn Val Asn Arg Lys Phe Lys Ser
        35                  40                  45

Pro Arg Ser Leu Ser Val Arg Ala Ser Ser Thr Ser Asp Ser Val Val
    50                  55                  60

Thr Leu Leu Asp Tyr Gly Ala Gly Asn Val Arg Ser Ile Arg Asn Ala
65                  70                  75                  80

Leu Arg His Leu Gly Phe Ser Ile Lys Asp Val Gln Thr Pro Gly Asp
                85                  90                  95

Ile Leu Asn Ala Asp Arg Leu Ile Phe Pro Gly Val Gly Pro Phe Ala
            100                 105                 110

Pro Ala Met Asp Val Leu Asn Arg Thr Gly Met Ala Glu Ala Leu Cys
        115                 120                 125

Lys Tyr Ile Glu Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu
    130                 135                 140

Gln Leu Leu Phe Asp Ser Ser Glu Gln Asn Gly Pro Val Lys Gly Leu
145                 150                 155                 160

Gly Val Ile Pro Gly Ile Val Gly Arg Phe Asp Ala Ser Ala Gly Ile
                165                 170                 175

Arg Val Pro His Ile Gly Trp Asn Ala Leu Gln Val Gly Lys Asp Ser
            180                 185                 190

Glu Ile Leu Asp Asp Val Gly Asn Arg His Val Tyr Phe Val His Ser
        195                 200                 205

Tyr Arg Ala Ile Pro Ser Asp Glu Asn Lys Asp Trp Ile Ser Ser Thr
    210                 215                 220

Cys Asn Tyr Gly Glu Ser Phe Ile Ser Ser Ile Arg Arg Gly Asn Val
225                 230                 235                 240

His Ala Val Gln Phe His Pro Glu Lys Ser Gly Glu Val Gly Leu Ser
                245                 250                 255

Val Leu Arg Arg Phe Leu His Pro Lys Leu Pro Ala Thr Gln Lys Pro
            260                 265                 270

Met Glu Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu
        275                 280                 285

Asp Val Arg Thr Asn Asp Lys Gly Asp Leu Val Val Thr Lys Gly Asp
    290                 295                 300

Gln Tyr Asp Val Arg Glu Gln Ser Asn Glu Asn Glu Val Arg Asn Leu
305                 310                 315                 320

Gly Lys Pro Val Asp Leu Ala Gly Gln Tyr Tyr Lys Asp Gly Ala Asp
                325                 330                 335
```

Glu Ile Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly
340 345 350

Asp Leu Pro Met Ile Gln Val Leu Arg Gln Thr Ser Lys Asn Val Phe
355 360 365

Val Pro Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Ser
370 375 380

Gly Arg Tyr Tyr Ser Ser Leu Glu Val Ala Ala Glu Tyr Phe Arg Ser
385 390 395 400

Gly Ala Asp Lys Met Ser Ile Gly Ser Asp Ala Val Phe Ala Ala Glu
405 410 415

Glu Phe Ile Lys Ser Gly Val Lys Thr Gly Lys Ser Ser Leu Glu Gln
420 425 430

Ile Ser Arg Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro
435 440 445

Arg Arg Val Tyr Val Asn His Pro Asp Asp Val Pro Tyr Lys Val Ile
450 455 460

Arg Val Thr Asn Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln
465 470 475 480

Cys Thr Val Ser Gly Gly Gln Glu Gly Arg Pro Ile Gly Ala Phe Glu
485 490 495

Leu Ala Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn
500 505 510

Cys Ile Asn Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Val
515 520 525

Lys Leu Ile Ser Asp Ser Val Gly Ile Pro Val Ile Ala Ser Ser Gly
530 535 540

Ala Gly Thr Pro Asp His Phe Ser Glu Val Phe Glu Glu Asp Lys Arg
545 550 555 560

Ile Cys Arg Ala Cys Cys Arg His Phe Pro Pro Glu Arg Gly Tyr Gln
565 570 575

Ser Gln Ser Val Lys Glu His Leu Gln Glu Glu Arg Ile Glu Val Arg
580 585 590

Ile